

SEQUENCE LISTING

<110> MOCKEL, BETTINA

BATHE, BRIGITTE

HANS, STEFAN

KREUTZER, CAROLINE

HERMANN, THOMAS

PFEFFERLE, WALTER

BINDER, MICHAEL

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<151> 2001-02-16

<150> DE 10162386.0

<151> 2001-12-19

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<213> Corynebacterium glutamicum

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Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr Lys
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Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu Glu Leu Ser Pro Ile	
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Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val Arg Asp Gly Asp Ile	
775 780 785	
ctg gtc ggt aag gtc acc cct aag ggc gag acc gag ctc acc ccg gaa	3116
Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr Glu Leu Thr Pro Glu	
790 795 800 805	
gag cgc ttg ctg cgc gca atc ttc ggt gag aag gcc cgc gaa gtt cgc	3164
Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys Ala Arg Glu Val Arg	
810 815 820	
gat acc tcc atg aag gtg cct cac ggt gag acc ggc aag gtc atc ggc	3212
Asp Thr Ser Met Lys Val Pro His Gly Glu Thr Gly Lys Val Ile Gly	
825 830 835	
gtg cgt cac ttc tcc cgc gag gac gac gac gat ctg gct cct ggc gtc	3260
Val Arg His Phe Ser Arg Glu Asp Asp Asp Asp Leu Ala Pro Gly Val	
840 845 850	
aac gag atg atc cgt atc tac gtt gct cag aag cgt aag atc cag gac	3308
Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys Arg Lys Ile Gln Asp	
855 860 865	
ggc gat aag ctc gct ggc cgc cac ggt aac aag ggt gtt gtc ggt aaa	3356
Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys Gly Val Val Gly Lys	
870 875 880 885	
att ttg cct cag gaa gat atg cca ttc ctt cca gac ggc act cct gtt	3404
Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro Asp Gly Thr Pro Val	
890 895 900	
gac atc atc ttg aac acc cac ggt gtt cca cgt cgt atg aac att ggt	3452
Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn Ile Gly	
905 910 915	
cag gtt ctt gag acc cac ctt ggc tgg ctg gca tct gct ggt tgg tcc	3500
Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly Trp Ser	
920 925 930	
gtg gat cct gaa gat cct gag aac gct gag ctc gtc aag act ctg cct	3548
Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr Leu Pro	
935 940 945	

gca gac ctc ctc gag gtt cct gct ggt tcc ttg act gca act cct gtg	3596
Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr Pro Val	
950 955 960 965	
ttc gac ggt gcg tca aac gaa gag ctc gca ggc ctg ctc gct aat tca	3644
Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala Asn Ser	
970 975 980	
cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt aaa gca	3692
Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly Lys Ala	
985 990 995	
acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg gtt	3737
Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro Val	
1000 1005 1010	
tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac	3782
Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp	
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Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr	
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Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe	
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Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr	
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aca ctt cag gag ctg ctg acc atc aag tct gat gac gtg gtt ggc	3962
Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp Asp Val Val Gly	
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cgt gtc aag gtc tac gaa gca att gtg aag ggc gag aac atc ccg	4007
Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly Glu Asn Ile Pro	
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gat cca ggt att cct gag tcc ttc aag gtt ctc ctc aag gag ctc	4052
Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu Leu Lys Glu Leu	
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Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser Ala Asp Gly Thr	
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cca atg gag ctc gcg ggt gac gac gac gac ttc gat cag gca ggc	4142
Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe Asp Gln Ala Gly	
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gcc tca ctt	ggc atc aac ctg tcc	cgt gac gag cgt tcc	gac gcc	4187
Ala Ser Leu	Gly Ile Asn Leu Ser	Arg Asp Glu Arg Ser	Asp Ala	
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gac acc gca tagcagatca gaaaacaacc gctagaaatc aagccataca				4236
Asp Thr Ala				
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<210> 6

<211> 1165

<212> PRT

<213> Corynebacterium glutamicum

<400> 6

Val Leu Glu Gly Pro Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val

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Val Asp Ile Pro Gly Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser	20	25	30
Ala Pro Ile Glu Val Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr	35	40	45
Ser Trp Leu Ile Gly Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu	50	55	60
Phe Gly Glu Gly Ala Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu	65	70	75
Glu Leu Ser Pro Ile Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu	85	90	95
Ser Glu Pro Arg Phe Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys	100	105	110
Glu Lys Asp Ile Asn Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe	115	120	125
Val Asn Asn Thr Thr Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly	130	135	140
Asp Phe Pro Met Met Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr	145	150	155
Glu Arg Val Val Val Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe	165	170	175
Asp Gln Thr Ile Asp Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys	180	185	190
Val Ile Pro Ser Arg Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg	195	200	205
Asp Ser Val Gly Val Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr			

210		215		220
Val Leu Leu Lys Ala Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg				
225		230		235
Phe Gly Phe Ser Glu Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val				
		245		250
Ala Asn Thr Asp Glu Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro				
		260		265
Gly Glu Gln Pro Thr Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser				
		275		280
Phe Phe Arg Ala Lys Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys				
		290		295
Ile Asn Arg Lys Leu Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr				
305		310		315
Leu Thr Glu Glu Asp Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu				
		325		330
His Ala Gly Glu Arg Val Met Thr Ser Pro Asn Gly Glu Glu Ile Pro				
		340		345
Val Glu Thr Asp Asp Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr				
		355		360
Val Gly Glu Leu Ile Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met				
		370		375
Glu Arg Val Val Arg Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile				
385		390		395
Thr Pro Thr Ser Leu Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg				
		405		410
Glu Phe Phe Gly Thr Ser Gln Leu Ser Gln Phe Met Val Gln Asn Asn				

420

425

430

Ser Leu Ser Gly Leu Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro
 435 440 445

Gly Gly Leu Ser Arg Glu Arg Ala Gly Ile Glu Val Arg Asp Val His
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Pro Ser His Tyr Gly Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro
 465 470 475 480

Asn Ile Gly Leu Ile Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro
 485 490 495

Phe Gly Phe Ile Glu Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu
 500 505 510

Thr Asp Gln Ile Asp Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val
 515 520 525

Val Ala Gln Ala Asn Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp
 530 535 540

Glu Thr Val Thr Val Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly
 545 550 555 560

Arg Asn Ala Val Asp Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser
 565 570 575

Val Gly Thr Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg
 580 585 590

Ala Leu Met Gly Ala Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg
 595 600 605

Ala Glu Ala Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr
 610 615 620

Asp Ala Gly Asp Leu Val Ile Thr Pro Val Ala Gly Val Val Glu Asn

625					630					635					640
Val	Ser	Ala	Asp	Phe	Ile	Thr	Ile	Met	Ala	Asp	Asp	Gly	Lys	Arg	Glu
				645					650					655	
Thr	Tyr	Leu	Leu	Arg	Lys	Phe	Gln	Arg	Thr	Asn	Gln	Gly	Thr	Ser	Tyr
			660					665					670		
Asn	Gln	Lys	Pro	Leu	Val	Asn	Leu	Gly	Glu	Arg	Val	Glu	Ala	Gly	Gln
		675					680					685			
Val	Ile	Ala	Asp	Gly	Pro	Gly	Thr	Phe	Asn	Gly	Glu	Met	Ser	Leu	Gly
690						695					700				
Arg	Asn	Leu	Leu	Val	Ala	Phe	Met	Pro	Trp	Glu	Gly	His	Asn	Tyr	Glu
705					710					715					720
Asp	Ala	Ile	Ile	Leu	Asn	Gln	Asn	Ile	Val	Glu	Gln	Asp	Ile	Leu	Thr
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Ser	Ile	His	Ile	Glu	Glu	His	Glu	Ile	Asp	Ala	Arg	Asp	Thr	Lys	Leu
			740					745					750		
Gly	Ala	Glu	Glu	Ile	Thr	Arg	Asp	Ile	Pro	Asn	Val	Ser	Glu	Glu	Val
		755					760					765			
Leu	Lys	Asp	Leu	Asp	Asp	Arg	Gly	Ile	Val	Arg	Ile	Gly	Ala	Asp	Val
	770					775					780				
Arg	Asp	Gly	Asp	Ile	Leu	Val	Gly	Lys	Val	Thr	Pro	Lys	Gly	Glu	Thr
785					790					795					800
Glu	Leu	Thr	Pro	Glu	Glu	Arg	Leu	Leu	Arg	Ala	Ile	Phe	Gly	Glu	Lys
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Ala	Arg	Glu	Val	Arg	Asp	Thr	Ser	Met	Lys	Val	Pro	His	Gly	Glu	Thr
			820					825					830		
Gly	Lys	Val	Ile	Gly	Val	Arg	His	Phe	Ser	Arg	Glu	Asp	Asp	Asp	Asp

835

840

845

Leu Ala Pro Gly Val Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys
 850 855 860

Arg Lys Ile Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys
 865 870 875 880

Gly Val Val Gly Lys Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro
 885 890 895

Asp Gly Thr Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg
 900 905 910

Arg Met Asn Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala
 915 920 925

Ser Ala Gly Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu
 930 935 940

Val Lys Thr Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu
 945 950 955 960

Thr Ala Thr Pro Val Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly
 965 970 975

Leu Leu Ala Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn
 980 985 990

Ala Asp Gly Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr
 995 1000 1005

Pro Tyr Pro Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His
 1010 1015 1020

His Leu Val Asp Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr
 1025 1030 1035

Ser Met Ile Thr Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly

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Gly Gln Arg Phe Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr				
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Gly Ala Ala Tyr Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp				
1070		1075		1080
Asp Val Val Gly Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly				
1085		1090		1095
Glu Asn Ile Pro Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu				
1100		1105		1110
Leu Lys Glu Leu Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser				
1115		1120		1125
Ala Asp Gly Thr Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe				
1130		1135		1140
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<211> 151

<212> DNA

<213> Corynebacterium glutamicum

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<210> 8

<211> 1926

<212> DNA

<213> Corynebacterium glutamicum

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<211> 1594

<212> DNA

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<220>

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<220>

<221> allele

<222> (659)..(1039)

<223> rpsL-1545 allele

<220>

<221> mutation

<222> (86)..(86)

<223> a to g

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<211> 20

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<213> Artificial sequence

<220>

<223> Synthetic DNA

<400> 10

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<210> 11

<211> 20

<212> DNA

<213> Corynebacterium glutamicum

<400> 11

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<210> 12

<211> 28

<212> DNA

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<210> 13

<211> 28

<212> DNA

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<210> 14

<211> 20

<212> DNA

<213> Corynebacterium glutamicum

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